

I. AMENDMENTS

AMENDMENTS TO THE CLAIMS

The listing of claims will replace all prior versions and listings of claims in the application:

1-65. (Canceled)

66. (Currently amended) A method for predicting the likelihood that a human colon cancer patient will exhibit a clinically beneficial patient response to treatment with ~~an inhibitor of ErbB1 activation~~ cetuximab, the method comprising:

a) assaying a normalized level of a predictive RNA transcript in a sample comprising ErbB1-expressing colon cancer cells obtained from said patient, wherein the predictive RNA transcript is the transcript of laminin gamma 2 (LAMC2);

b) analyzing the normalized level of the LAMC2 transcript; and

c) predicting the likelihood of response of the patient to treatment with ~~the inhibitor of ErbB1 activation~~ cetuximab based on the normalized level of the LAMC2 transcript, wherein an increased normalized level of LAMC2 RNA transcript correlates with resistance of the colon cancer to treatment with ~~the inhibitor of ErbB1 activation~~ cetuximab, ~~wherein the inhibitor of ErbB1 activation is a monoclonal antibody that binds to ErbB1.~~

67. (Canceled)

68. (Previously presented) The method of claim 66, wherein said sample is a tissue sample.

69. (Previously presented) The method of claim 68, wherein the tissue sample is fixed, paraffin-embedded, or fresh, or frozen.

70. (Previously presented) The method of claim 68, wherein the tissue sample is derived from fine needle, core, or other types of biopsy.

71. (Currently amended) The method of claim 66, further comprising the step of preparing a report comprising a statement whether the patient is likely to respond to treatment with ~~the inhibitor of ErbB1 activation~~ cetuximab.

72. (Previously presented) The method of claim 66, wherein the normalized level of the LAMC2 RNA transcript is determined using an array comprising polynucleotides hybridizing to a LAMC2 gene immobilized on a solid surface.

73. (Previously presented) The method of claim 72, wherein said polynucleotides are cDNAs.

74. (Previously presented) The method of claim 73, wherein said cDNAs are about 500 to about 5000 bases.

75. (Previously presented) The method of claim 72, wherein said polynucleotides are oligonucleotides.

76. (Previously presented) The method of claim 75, wherein said oligonucleotides are about 20 to 80 bases long.

77. (Previously presented) The method of claim 72, wherein the array comprises about 330,000 oligonucleotides.

78. (Previously presented) The method of claim 72 wherein said solid surface is glass.

79. (Previously presented) The method of claim 68, wherein RNA is isolated from colon cancer cells present in a fixed, paraffin-embedded tissue by a procedure comprising:

(a) incubating one or more sections of said fixed, paraffin-embedded tissue at a temperature of about 56 °C to 70 °C in a lysis buffer, in the presence of a protease, without prior dewaxing, to form a lysis solution;

(b) cooling the lysis solution to a temperature where the paraffin solidifies, thereby generating a cooled lysis solution; and

(c) isolating the RNA from said cooled lysis solution.

80. (Previously presented) The method of claim 66, further comprising the use of a kit comprising one or more of (1) extraction buffer/reagents for extracting mRNA from a sample and protocol; (2) reverse transcription buffer/reagents and protocol; and (3) quantitative polymerase chain reaction (qPCR) buffer/reagents and protocol suitable for performing the method of claim 66.

81. (Previously presented) The method of claim 72, wherein said polynucleotides comprise modified and unmodified polynucleotides.

82. (Currently amended) The method of claim 66, further comprising determining the normalized level of one or more predictive RNA transcripts in said sample, wherein the predictive RNA transcript is the transcript of one or more genes selected from the group consisting of: ErbB3; EREG; ID1; TITF1; CA9; CD44v6; DR5; KRT17; P14ARF; and PLAUR, wherein an increased normalized level of the predictive RNA transcript of one or more of CA9; CD44v6; DR5; KRT17; P14ARF; and PLAUR, indicates that the patient will show a decreased likelihood of response to treatment with ~~the~~ ErbB1-inhibitor cetuximab, and an increased normalized level of the predictive RNA transcript of one or more of ErbB3; EREG; ID1; and TITF1 indicates that the patient will show an increased likelihood of response to treatment with ~~the inhibitor of ErbB1-activation~~ cetuximab.

83. (Previously presented) The method of claim 66, further comprising determining the normalized level of a predictive RNA transcript of KRT17 in the sample.